

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 08/989,896  
Source: IFWO  
Date Processed by STIC: 09/12-2005

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IFWO

**RAW SEQUENCE LISTING**

PATENT APPLICATION: US/08/989,896

DATE: 09/12/2005

TIME: 12:57:56

Input Set : N:\CrF3\RULE60\08989896.raw.txt  
 Output Set: N:\CRF4\09092005\H989896.raw

**SEQUENCE LISTING**

## 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Gehrmann, Mathias  
 6 Seemann, Gerhard  
 7 Bosslet, Klaus  
 8 Czech, Joerg

10 (ii) TITLE OF INVENTION: Fusion Protein for Prodrug Activity

12 (iii) NUMBER OF SEQUENCES: 18

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
 16 Dunner  
 17 (B) STREET: 1300 I Street, N.W.  
 18 (C) CITY: Washington  
 19 (D) STATE: D.C.  
 20 (E) COUNTRY: USA  
 21 (F) ZIP: 20005-3315

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk  
 25 (B) COMPUTER: IBM PC compatible  
 26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

29 (vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: US/08/989,896  
 C--> 31 (B) FILING DATE: 12-Dec-1997

33 (vii) PRIOR APPLICATION DATA:

W--> 34 (A) APPLICATION NUMBER: US/08/475,826  
 35 (B) FILING DATE: 07-JUN-1995

W--> 36 (A) APPLICATION NUMBER: US 08/129,379  
 37 (B) FILING DATE: 30-SEP-1993

W--> 39 (A) APPLICATION NUMBER: DE P 42 33 152.8  
 40 (B) FILING DATE: 02-OCT-1992

42 (viii) ATTORNEY/AGENT INFORMATION:

43 (A) NAME: Barker, M. P.  
 44 (B) REGISTRATION NUMBER: 32,013  
 45 (C) REFERENCE/DOCKET NUMBER: 02481.1337-00000

47 (ix) TELECOMMUNICATION INFORMATION:

48 (A) TELEPHONE: 202-408-4000  
 49 (B) TELEFAX: 202-408-4400

52 (2) INFORMATION FOR SEQ ID NO: 1:

54 (i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 3314 base pairs  
 56 (B) TYPE: nucleic acid  
 57 (C) STRANDEDNESS: single

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58 (D) TOPOLOGY: linear  
 60 (ii) MOLECULE TYPE: DNA (genomic)  
 63 (ix) FEATURE:  
 64 (A) NAME/KEY: sig\_peptide  
 65 (B) LOCATION: 145..283  
 67 (ix) FEATURE:  
 68 (A) NAME/KEY: mat\_peptide  
 69 (B) LOCATION: join(284..1003, 1069..1119, 1263..3161)  
 71 (ix) FEATURE:  
 72 (A) NAME/KEY: CDS  
 73 (B) LOCATION: join(145..189, 272..1003, 1069..1119, 1263..3161)  
 76 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 78 CCAAGCTTAT GAATATGCAA ATCCTGCTCA TGAATATGCA AATCCTCTGA ATCTACATGG 60  
 80 TAAATATAGG TTTGTCTATA CCACAAACAG AAAAACATGA GATCACAGTT CTCTCTACAG 120  
 82 TTACTGAGCA CACAGGACCT CACC ATG GGA TGG AGC TGT ATC ATC CTC TTC 171  
 83 Met Gly Trp Ser Cys Ile Ile Leu Phe  
 84 -19 -15  
 86 TTG GTA GCA ACA GCT ACA GGTAAGGGGC TCACAGTAGC AGGCTTGAGG 219  
 87 Leu Val Ala Thr Ala Thr  
 88 -10 -5  
 90 TCTGGACATA TATATGGGTG ACAATGACAT CCACTTGCC TTTCTCTCCA CA GGT 274  
 91 Gly  
 92 -4  
 94 GTC CAC TCC CAG GTC CAA CTG CAG GAG AGC GGT CCA GGT CTT GTG AGA 322  
 95 Val His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg  
 96 1 5 10  
 98 CCT AGC CAG ACC CTG AGC CTG ACC TGC ACC GTG TCT GGC TTC ACC ATC 370  
 99 Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Thr Ile  
 100 15 20 25  
 102 AGC AGT GGT TAT AGC TGG CAC TGG GTG AGA CAG CCA CCT GGA CGA GGT 418  
 103 Ser Ser Gly Tyr Ser Trp His Trp Val Arg Gln Pro Pro Gly Arg Gly  
 104 30 35 40 45  
 106 CTT GAG TGG ATT GGA TAC ATA CAG TAC AGT GGT ATC ACT AAC TAC AAC 466  
 107 Leu Glu Trp Ile Gly Tyr Ile Gln Tyr Ser Gly Ile Thr Asn Tyr Asn  
 108 50 55 60  
 110 CCC TCT CTC AAA AGT AGA GTG ACA ATG CTG GTA GAC ACC AGC AAG AAC 514  
 111 Pro Ser Leu Lys Ser Arg Val Thr Met Leu Val Asp Thr Ser Lys Asn  
 112 65 70 75  
 114 CAG TTC AGC CTG AGA CTC AGC AGC GTG ACA GCC GCC GAC ACC GCG GTC 562  
 115 Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
 116 80 85 90  
 118 TAT TAT TGT GCA AGA GAA GAC TAT GAT TAC CAC TGG TAC TTC GAT GTC 610  
 119 Tyr Tyr Cys Ala Arg Glu Asp Tyr Asp Tyr His Trp Tyr Phe Asp Val  
 120 95 100 105  
 122 TGG GGC CAA GGG ACC ACG GTC ACC GTC TCC TCA GGA GGC GGT GGA TCG 658  
 123 Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser  
 124 110 115 120 125  
 126 GGC GGT GGT GGG TCG GGT GGC GGC GGA TCT GAC ATC CAG CTG ACC CAG 706  
 127 Gly Gly Gly Ser Gly Gly Ser Asp Ile Gln Leu Thr Gln

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128	130	135	140	
130 AGC CCA AGC AGC CTG AGC GCC AGC GTG GGT GAC AGA GTG ACC ACC ATC ACC				754
131 Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr				
132 145	150	155		
134 TGT AGT ACC AGC TCG AGT GTA AGT TAC ATG CAC TGG TAC CAG CAG AAG				802
135 Cys Ser Thr Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys				
136 160	165	170		
138 CCA GGT AAG GCT CCA AAG CTG CTG ATC TAC AGC ACA TCC AAC CTG GCT				850
139 Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Thr Ser Asn Leu Ala				
140 175	180	185		
142 TCT GGT GTG CCA AGC AGA TTC AGC GGT AGC GGT ACC GAC TTC				898
143 Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe				
144 190	195	200	205	
146 ACC TTC ACC ATC AGC AGC CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC				946
147 Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr				
148 210	215	220		
150 TGC CAT CAG TGG AGT AGT TAT CCC ACG TTC GGC CAA GGG ACC AAG CTG				994
151 Cys His Gln Trp Ser Ser Tyr Pro Thr Phe Gly Gln Gly Thr Lys Leu				
152 225	230	235		
154 GAG ATC AAA GGTGAGTAGA ATTTAAACTT TGCTTCCTCA GTTGGATCTG				1043
155 Glu Ile Lys				
156 240				
158 AGTAACCTCCC AATCTTCTCT CTGCA GAG CTC AAA ACC CCA CTT GGT GAC ACA				1095
159 Glu Leu Lys Thr Pro Leu Gly Asp Thr				
160 245				
162 ACT CAC ACA TGC CCA CGG TGC CCA GGTAAGCCAG CCCAGGACTC GCCCTCCAGC				1149
163 Thr His Thr Cys Pro Arg Cys Pro				
164 250	255			
166 TCAAGGCGGG ACAAGAGCCC TAGAGTGGCC TGAGTCCAGG GACAGGCCAG AGCAGGGTG				1209
168 TGACGCATCC ACCTCCATCC CAGATCCCCG TAACTCCCAA TCTTCTCTCT GCA GCG				1265
169 Ala				
172 GCG GCG GCG GTG CAG GGC GGG ATG CTG TAC CCC CAG GAG AGC CCG TCG				1313
173 Ala Ala Ala Val Gln Gly Gly Met Leu Tyr Pro Gln Glu Ser Pro Ser				
174 260	265	270		
176 CGG GAG TGC AAG GAG CTG GAC GGC CTC TGG AGC TTC CGC GCC GAC TTC				1361
177 Arg Glu Cys Lys Glu Leu Asp Gly Leu Trp Ser Phe Arg Ala Asp Phe				
178 275	280	285	290	
180 TCT GAC AAC CGA CGC CGG GGC TTC GAG GAG CAG TGG TAC CGG CGG CCG				1409
181 Ser Asp Asn Arg Arg Gly Phe Glu Glu Gln Trp Tyr Arg Arg Pro				
182 295	300	305		
184 CTG TGG GAG TCA GGC CCC ACC GTG GAC ATG CCA GTT CCC TCC AGC TTC				1457
185 Leu Trp Glu Ser Gly Pro Thr Val Asp Met Pro Val Pro Ser Ser Phe				
186 310	315	320		
188 AAT GAC ATC AGC CAG GAC TGG CGT CTG CGG CAT TTT GTC GGC TGG GTG				1505
189 Asn Asp Ile Ser Gln Asp Trp Arg Leu Arg His Phe Val Gly Trp Val				
190 325	330	335		
192 TGG TAC GAA CGG GAG GTG ATC CTG CCG GAG CGA TGG ACC CAG GAC CTG				1553
193 Trp Tyr Glu Arg Glu Val Ile Leu Pro Glu Arg Trp Thr Gln Asp Leu				
194 340	345	350		

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196	CGC ACA AGA GTG GTG CTG AGG ATT GGC AGT GCC CAT TCC TAT GCC ATC	1601
197	Arg Thr Arg Val Val Leu Arg Ile Gly Ser Ala His Ser Tyr Ala Ile	
198	355 360 365 370	
200	GTG TGG GTG AAT GGG GTC GAC ACG CTA GAG CAT GAG GGG GGC TAC CTC	1649
201	Val Trp Val Asn Gly Val Asp Thr Leu Glu His Glu Gly Gly Tyr Leu	
202	375 380 385	
204	CCC TTC GAG GCC GAC ATC AGC AAC CTG GTC CAG GTG GGG CCC CTG CCC	1697
205	Pro Phe Glu Ala Asp Ile Ser Asn Leu Val Gln Val Gly Pro Leu Pro	
206	390 395 400	
208	TCC CGG CTC CGA ATC ACT ATC GCC ATC AAC ACA CTC ACC CCC ACC	1745
209	Ser Arg Leu Arg Ile Thr Ile Ala Ile Asn Asn Thr Leu Thr Pro Thr	
210	405 410 415	
212	ACC CTG CCA CCA GGG ACC ATC CAA TAC CTG ACT GAC ACC TCC AAG TAT	1793
213	Thr Leu Pro Pro Gly Thr Ile Gln Tyr Leu Thr Asp Thr Ser Lys Tyr	
214	420 425 430	
216	CCC AAG GGT TAC TTT GTC CAG AAC ACA TAT TTT GAC TTT TTC AAC TAC	1841
217	Pro Lys Gly Tyr Phe Val Gln Asn Thr Tyr Phe Asp Phe Phe Asn Tyr	
218	435 440 445 450	
220	GCT GGA CTG CAG CGG TCT GTA CTT CTG TAC ACG ACA CCC ACC ACC TAC	1889
221	Ala Gly Leu Gln Arg Ser Val Leu Leu Tyr Thr Thr Pro Thr Thr Tyr	
222	455 460 465	
224	ATC GAT GAC ATC ACC GTC ACC ACC AGC GTG GAG CAA GAC AGT GGG CTG	1937
225	Ile Asp Asp Ile Thr Val Thr Ser Val Glu Gln Asp Ser Gly Leu	
226	470 475 480	
228	GTG AAT TAC CAG ATC TCT GTC AAG GGC AGT AAC CTG TTC AAG TTG GAA	1985
229	Val Asn Tyr Gln Ile Ser Val Lys Gly Ser Asn Leu Phe Lys Leu Glu	
230	485 490 495	
232	GTG CGT CTT TTG GAT GCA GAA AAC AAA GTC GTG GCG AAT GGG ACT GGG	2033
233	Val Arg Leu Leu Asp Ala Glu Asn Lys Val Val Ala Asn Gly Thr Gly	
234	500 505 510	
236	ACC CAG GGC CAA CTT AAG GTG CCA GGT GTC AGC CTC TGG TGG CCG TAC	2081
237	Thr Gln Gly Gln Leu Lys Val Pro Gly Val Ser Leu Trp Trp Pro Tyr	
238	515 520 525 530	
240	CTG ATG CAC GAA CGC CCT GCC TAT CTG TAT TCA TTG GAG GTG CAG CTG	2129
241	Leu Met His Glu Arg Pro Ala Tyr Leu Tyr Ser Leu Glu Val Gln Leu	
242	535 540 545	
244	ACT GCA CAG ACG TCA CTG GGG CCT GTG TCT GAC TTC TAC ACA CTC CCT	2177
245	Thr Ala Gln Thr Ser Leu Gly Pro Val Ser Asp Phe Tyr Thr Leu Pro	
246	550 555 560	
248	GTG GGG ATC CGC ACT GTG GCT GTC ACC AAG AGC CAG TTC CTC ATC AAT	2225
249	Val Gly Ile Arg Thr Val Ala Val Thr Lys Ser Gln Phe Leu Ile Asn	
250	565 570 575	
252	GGG AAA CCT TTC TAT TTC CAC GGT GTC AAC AAG CAT GAG GAT GCG GAC	2273
253	Gly Lys Pro Phe Tyr Phe His Gly Val Asn Lys His Glu Asp Ala Asp	
254	580 585 590	
256	ATC CGA GGG AAG GGC TTC GAC TGG CCG CTG CTG GTG AAG GAC TTC AAC	2321
257	Ile Arg Gly Lys Gly Phe Asp Trp Pro Leu Leu Val Lys Asp Phe Asn	
258	595 600 605 610	
260	CTG CTT CGC TGG CTT GGT GCC AAC GCT TTC CGT ACC AGC CAC TAC CCC	2369

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261	Leu	Leu	Arg	Trp	Leu	Gly	Ala	Asn	Ala	Phe	Arg	Thr	Ser	His	Tyr	Pro	
262					615					620						625	
264	TAT	GCA	GAG	GAA	GTG	ATG	CAG	ATG	TGT	GAC	CGC	TAT	GGG	ATT	GTG	GTC	2417
265	Tyr	Ala	Glu	Glu	Val	Met	Gln	Met	Cys	Asp	Arg	Tyr	Gly	Ile	Val	Val	
266					630				635						640		
268	ATC	GAT	GAG	TGT	CCC	GGC	GTG	GGC	CTG	GCG	CTG	CCG	CAG	TTC	TTC	AAC	2465
269	Ile	Asp	Glu	Cys	Pro	Gly	Val	Gly	Leu	Ala	Leu	Pro	Gln	Phe	Phe	Asn	
270					645				650				655				
272	AAC	GTT	TCT	CTG	CAT	CAC	CAC	ATG	CAG	GTG	ATG	GAA	GAA	GTG	GTG	CGT	2513
273	Asn	Val	Ser	Leu	His	His	His	Met	Gln	Val	Met	Glu	Glu	Val	Val	Arg	
274					660				665			670					
276	AGG	GAC	AAG	AAC	CAC	CCC	GCG	GTC	GTG	ATG	TGG	TCT	GTG	GCC	AAC	GAG	2561
277	Arg	Asp	Lys	Asn	His	Pro	Ala	Val	Val	Met	Trp	Ser	Val	Ala	Asn	Glu	
278	675				680				685				690				
280	CCT	GCG	TCC	CAC	CTA	GAA	TCT	GCT	GGC	TAC	TAC	TTG	AAG	ATG	GTG	ATC	2609
281	Pro	Ala	Ser	His	Leu	Glu	Ser	Ala	Gly	Tyr	Tyr	Leu	Lys	Met	Val	Ile	
282					695				700			705					
284	GCT	CAC	ACC	AAA	TCC	TTG	GAC	CCC	TCC	CGG	CCT	GTG	ACC	TTT	GTG	AGC	2657
285	Ala	His	Thr	Lys	Ser	Leu	Asp	Pro	Ser	Arg	Pro	Val	Thr	Phe	Val	Ser	
286					710				715			720					
288	AAC	TCT	AAC	TAT	GCA	GCA	GAC	AAG	GGG	GCT	CCG	TAT	GTG	GAT	GTG	ATC	2705
289	Asn	Ser	Asn	Tyr	Ala	Ala	Asp	Lys	Gly	Ala	Pro	Tyr	Val	Asp	Val	Ile	
290					725				730			735					
292	TGT	TTG	AAC	AGC	TAC	TAC	TCT	TGG	TAT	CAC	GAC	TAC	GGG	CAC	CTG	GAG	2753
293	Cys	Leu	Asn	Ser	Tyr	Tyr	Ser	Trp	Tyr	His	Asp	Tyr	Gly	His	Leu	Glu	
294					740				745			750					
296	TTG	ATT	CAG	CTG	CAG	CTG	GCC	ACC	CAG	TTT	GAG	AAC	TGG	TAT	AAG	AAG	2801
297	Leu	Ile	Gln	Leu	Gln	Leu	Ala	Thr	Gln	Phe	Glu	Asn	Trp	Tyr	Lys	Lys	
298	755				760				765			770					
300	TAT	CAG	AAG	CCC	ATT	ATT	CAG	AGC	GAG	TAT	GGA	GCA	GAA	ACG	ATT	GCA	2849
301	Tyr	Gln	Lys	Pro	Ile	Ile	Gln	Ser	Glu	Tyr	Gly	Ala	Glu	Thr	Ile	Ala	
302					775				780			785					
304	GGG	TTT	CAC	CAG	GAT	CCA	CCT	CTG	ATG	TTC	ACT	GAA	GAG	TAC	CAG	AAA	2897
305	Gly	Phe	His	Gln	Asp	Pro	Pro	Leu	Met	Phe	Thr	Glu	Glu	Tyr	Gln	Lys	
306					790				795			800					
308	AGT	CTG	CTA	GAG	CAG	TAC	CAT	CTG	GGT	CTG	GAT	CAA	AAA	CGC	AGA	AAA	2945
309	Ser	Leu	Leu	Glu	Gln	Tyr	His	Leu	Gly	Leu	Asp	Gln	Lys	Arg	Arg	Lys	
310					805				810			815					
312	TAT	GTG	GTT	GGA	GAG	CTC	ATT	TGG	AAT	TTT	GCC	GAT	TTC	ATG	ACT	GAA	2993
313	Tyr	Val	Val	Gly	Glu	Leu	Ile	Trp	Asn	Phe	Ala	Asp	Phe	Met	Thr	Glu	
314					820				825			830					
316	CAG	TCA	CCG	ACG	AGA	GTG	CTG	GGG	ATT	AAA	AAG	GGG	ATC	TTC	ACT	CGG	3041
317	Gln	Ser	Pro	Thr	Arg	Val	Leu	Gly	Asn	Lys	Lys	Gly	Ile	Phe	Thr	Arg	
318	835				840				845			850					
320	CAG	AGA	CAA	CCA	AAA	AGT	GCA	GCG	TTC	CTT	TTG	CGA	GAG	AGA	TAC	TGG	3089
321	Gln	Arg	Gln	Pro	Lys	Ser	Ala	Ala	Phe	Leu	Leu	Arg	Glu	Arg	Tyr	Trp	
322					855				860			865					
324	AAG	ATT	GCC	AAT	GAA	ACC	AGG	TAT	CCC	CAC	TCA	GTA	GCC	AAG	TCA	CAA	3137
325	Lys	Ile	Ala	Asn	Glu	Thr	Arg	Tyr	Pro	His	Ser	Val	Ala	Lys	Ser	Gln	

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L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:36 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vii)  
L:39 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vii)